

SEQUENCE LISTING

<110> Shorrosh, Basil S.
DeBonte, Lorin R.

<120> PLANTS CONTAINING A CYTOSOLIC ACETYL
COA-CARBOXYLASE

<130> 07148-094001

<150> US 60/198,794

<151> 2000-04-20

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0003947, 042001

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Ser Arg His Pro Ala Thr Thr Thr Glu Val Asp Glu Tyr Cys Asn Ala	
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Leu Gly Gly Asn Lys Pro Ile His Ser Ile Leu Ile Ala Asn Asn Gly	
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Thr Phe Gly Thr Glu Lys Ala Ile Leu Leu Val Ala Met Ala Thr Pro	
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Glu Asp Met Arg Ile Asn Ala Glu His Ile Arg Ile Ala Asp Gln Phe	
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Val Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Gln	
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000240" 245360

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FOO240" 246860

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Pro Leu Ser Ile Tyr Leu Glu Leu Asp Lys Leu Lys Cys Tyr Glu Asn	
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FOUO 2440 04240

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ctt ggt agg gag gtg tac agc tct cac atg caa ctt ggt gga ccg aaa Leu Gly Arg Glu Val Tyr Ser Ser His Met Gln Leu Gly Gly Pro Lys 1780 1785 1790	5376

atc atg gca aca aat gga gtc gtt cat ctc aca gtt tcg gac gac ctt Ile Met Ala Thr Asn Gly Val Val His Leu Thr Val Ser Asp Asp Leu 1795 1800 1805	5424
gaa ggc gtt tct tct att ttg aag tgg ctt agc tac gtt cct tct cat Glu Gly Val Ser Ser Ile Leu Lys Trp Leu Ser Tyr Val Pro Ser His 1810 1815 1820	5472
gta ggt ggt gca ctt ccc att gta aag ccc ctt gat ccc cca gag agg Val Gly Gly Ala Leu Pro Ile Val Lys Pro Leu Asp Pro Pro Glu Arg 1825 1830 1835 1840	5520
gaa gtg gag tat tta ccg gaa aat tca tgc gat cct cgt gct gcc att Glu Val Glu Tyr Leu Pro Glu Asn Ser Cys Asp Pro Arg Ala Ala Ile 1845 1850 1855	5568
tcc gga act ctg gat gtt aat gga aag tgg ctg gga ggc att ttt gac Ser Gly Thr Leu Asp Val Asn Gly Lys Trp Leu Gly Gly Ile Phe Asp 1860 1865 1870	5616
aag gac agc ttt gtg gag aca cta gaa gga tgg gct aga aca gtt gtt Lys Asp Ser Phe Val Glu Thr Leu Glu Gly Trp Ala Arg Thr Val Val 1875 1880 1885	5664
aca gga agg gca aag ctt gga gga atc cct gtg gga att gtt gcg gtg Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro Val Gly Ile Val Ala Val 1890 1895 1900	5712
gaa aca caa aca gtt atg caa ata ata cct gct gat cca ggt caa ctt Glu Thr Gln Thr Val Met Gln Ile Ile Pro Ala Asp Pro Gly Gln Leu 1905 1910 1915 1920	5760
gat tct cac gag agg gtt gtt cct caa gcc ggg cag gtg tgg ttt cct Asp Ser His Glu Arg Val Val Pro Gln Ala Gly Gln Val Trp Phe Pro 1925 1930 1935	5808
gat tct gcg acc aag acg gcc caa gcg ata ttg gat ttc aac aga gaa Asp Ser Ala Thr Lys Thr Ala Gln Ala Ile Leu Asp Phe Asn Arg Glu 1940 1945 1950	5856
gaa ctc cca ctt ttc att atc gca aac tgg aga ggc ttt tca ggt gga Glu Leu Pro Leu Phe Ile Ile Ala Asn Trp Arg Gly Phe Ser Gly Gly 1955 1960 1965	5904
caa agg gac ctt ttt gaa gga att ctt cag gct ggt tcg act att gtg Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln Ala Gly Ser Thr Ile Val 1970 1975 1980	5952
gag aac ctt agg aca tac aaa cag ccc ata ttt gta tac att cca atg Glu Asn Leu Arg Thr Tyr Lys Gln Pro Ile Phe Val Tyr Ile Pro Met 1985 1990 1995 2000	6000
atg ggt gaa ctc cga ggc ggg gct tgg gtt gtt gtc gac agc cga atc Met Gly Glu Leu Arg Gly Gly Ala Trp Val Val Val Asp Ser Arg Ile 2005 2010 2015	6048
aac tca gac cac att gaa atg tat gct gag cga acg gcc aaa ggt aac	6096

0933947 "042004"

Asn Ser Asp His Ile Glu Met Tyr Ala Glu Arg Thr Ala Lys Gly Asn	
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gtc ctt gag ccg gaa gga atg att gaa atc aaa ttt aga aca aga gaa	6144
Val Leu Glu Pro Glu Gly Met Ile Glu Ile Lys Phe Arg Thr Arg Glu	
2035	2040 2045
ttg ttg gag tgt atg aga aga ctt gat caa caa ttg att aat ttg aag	6192
Leu Leu Glu Cys Met Arg Arg Leu Asp Gln Gln Leu Ile Asn Leu Lys	
2050	2055 2060
gaa aaa ctt tct gaa gcc aag agt aac aag gac tat ggt gca tat gat	6240
Glu Lys Leu Ser Glu Ala Lys Ser Asn Lys Asp Tyr Gly Ala Tyr Asp	
2065	2070 2075 2080
tct ctg cag cag cag att aga ttc cgt gag aaa cag ctt ttg cct ttg	6288
Ser Leu Gln Gln Gln Ile Arg Phe Arg Glu Lys Gln Leu Leu Pro Leu	
2085	2090 2095
tat act cag ata gct aca aaa ttt gct gaa ctc cat gat act tca tta	6336
Tyr Thr Gln Ile Ala Thr Lys Phe Ala Glu Leu His Asp Thr Ser Leu	
2100	2105 2110
aga atg aaa gca aag ggt gta atc aga gaa gtt ctt gat tgg cgt aag	6384
Arg Met Lys Ala Lys Gly Val Ile Arg Glu Val Leu Asp Trp Arg Lys	
2115	2120 2125
tcg cgt tct gtc ttc tat cag aga ctg cac agg aga atc ggt gag cac	6432
Ser Arg Ser Val Phe Tyr Gln Arg Leu His Arg Arg Ile Gly Glu His	
2130	2135 2140
tca ctg atc aac atc gtg aga gat gct gct ggt gac caa ttg tca tat	6480
Ser Leu Ile Asn Ile Val Arg Asp Ala Ala Gly Asp Gln Leu Ser Tyr	
2145	2150 2155 2160
gtt tct gcc atg aac ttg ctc aaa gaa tgg tat ctg aat tct gat atc	6528
Val Ser Ala Met Asn Leu Leu Lys Glu Trp Tyr Leu Asn Ser Asp Ile	
2165	2170 2175
gcc aaa ggt aga gaa gat gct tgg ttg gac gat gaa gcc ttc ttc aga	6576
Ala Lys Gly Arg Glu Asp Ala Trp Leu Asp Asp Glu Ala Phe Phe Arg	
2180	2185 2190
tgg agg gat gat cca gca aac tac gag gat aaa cta aag gaa ttg cgc	6624
Trp Arg Asp Asp Pro Ala Asn Tyr Glu Asp Lys Leu Lys Glu Leu Arg	
2195	2200 2205
gtc cag aga ctg ttg ctt cag ttg aca aat att ggc gac tcg gct cta	6672
Val Gln Arg Leu Leu Leu Gln Leu Thr Asn Ile Gly Asp Ser Ala Leu	
2210	2215 2220
gat tta caa gct cta cct caa ggt ctt gcc gcc ctt tta agc aag ttg	6720
Asp Leu Gln Ala Leu Pro Gln Gly Leu Ala Ala Leu Leu Ser Lys Leu	
2225	2230 2235 2240
gaa gca tca agt cgc gat aag ttg atc agt gaa ctt cgc aaa gta ctc	6768
Glu Ala Ser Ser Arg Asp Lys Leu Ile Ser Glu Leu Arg Lys Val Leu	

F00210" 42468660

2245

2250

2255

ggt tagtagacag tgaatgctcc tgtgatctgc ccatgcactc atgtttagt 6821
Gly

gttcacgtcg ttgatacatg accatataga aatgtatcca ttttacgatg ttatcatcaa 6881
agtagcagca tccctcggaa aatggacttt cacttgaggg atcaactgta aatgacttcg 6941
gtcttgata gatatttaatt ttatgcagtt agaggatcat aaccagcatc accatgtttg 7001
gtctatttat ttgctgggtg attgattcct tgcgtgtatc tgaataaaca tgtaataatt 7061
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<400> 8

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Ser	Arg	His	Pro	Ala	Thr	Thr	Thr	Glu	Val	Asp	Glu	Tyr	Cys	Asn	Ala
			20					25					30		
Leu	Gly	Gly	Asn	Lys	Pro	Ile	His	Ser	Ile	Leu	Ile	Ala	Asn	Asn	Gly
			35				40						45		
Met	Ala	Ala	Val	Lys	Phe	Ile	Arg	Ser	Val	Arg	Ser	Trp	Ala	Tyr	Glu
	50					55					60				
Thr	Phe	Gly	Thr	Glu	Lys	Ala	Ile	Leu	Leu	Val	Ala	Met	Ala	Thr	Pro
65					70					75					80
Glu	Asp	Met	Arg	Ile	Asn	Ala	Glu	His	Ile	Arg	Ile	Ala	Asp	Gln	Phe
				85					90					95	
Val	Glu	Val	Pro	Gly	Gly	Thr	Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Gln
			100				105						110		
Leu	Ile	Leu	Glu	Ile	Ala	Glu	Ile	Thr	His	Val	Asp	Ala	Val	Trp	Pro
	115						120					125			
Gly	Trp	Gly	His	Ala	Ser	Glu	Asn	Pro	Glu	Leu	Pro	Asp	Ala	Leu	Lys
	130					135					140				
Ala	Lys	Gly	Ile	Val	Phe	Leu	Gly	Pro	Pro	Ala	Ile	Ser	Met	Ala	Ala
145					150					155					160
Leu	Gly	Asp	Lys	Ile	Gly	Ser	Ser	Leu	Ile	Ala	Gln	Ala	Ala	Glu	Val
				165					170					175	
Pro	Thr	Leu	Pro	Trp	Ser	Gly	Ser	His	Val	Lys	Ile	Pro	Pro	Glu	Ser
			180					185					190		
Asp	Leu	Ile	Thr	Ile	Pro	Asp	Glu	Ile	Tyr	Arg	Ala	Ala	Cys	Val	Tyr
	195					200						205			
Thr	Thr	Glu	Glu	Ala	Ile	Ala	Ser	Cys	Gln	Val	Val	Gly	Tyr	Pro	Ala
	210					215						220			
Met	Ile	Lys	Ala	Ser	Trp	Gly	Gly	Gly	Gly	Lys	Gly	Ile	Arg	Lys	Val
225					230					235					240
His	Asn	Asp	Asp	Glu	Val	Arg	Ala	Leu	Phe	Lys	Gln	Val	Gln	Gly	Glu
				245					250					255	
Val	Pro	Gly	Ser	Pro	Ile	Phe	Ile	Met	Lys	Val	Ala	Ser	Gln	Ser	Arg
			260					265					270		
His	Leu	Glu	Val	Gln	Leu	Ile	Cys	Asp	Gln	His	Gly	Asn	Phe	Ala	Ala
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Leu	His	Ser	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His	Gln	Lys	Ile	Ile
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 Glu Gln Ala Ala Arg Arg Leu Ala Lys Ser Val Asn Tyr Val Gly Ala
 325 330 335
 Ala Thr Val Glu Tyr Leu Tyr Ser Met Glu Thr Gly Glu Tyr Tyr Phe
 340 345 350
 Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Trp
 355 360 365
 Ile Ala Glu Ile Asn Leu Pro Ala Ala Gln Val Ala Val Gly Met Gly
 370 375 380
 Ile Pro Leu Trp Gln Ile Pro Glu Ile Arg Arg Phe Tyr Gly Met Glu
 385 390 395 400
 His Gly Gly Gly Asn Asp Gly Trp Lys Lys Thr Ser Val Leu Ala Thr
 405 410 415
 Pro Phe Asp Phe Asp Glu Ala Gln Ser Thr Lys Pro Lys Gly His Cys
 420 425 430
 Val Ala Val Arg Val Thr Ser Glu Asp Pro Asp Asp Gly Phe Thr Pro
 435 440 445
 Thr Gly Gly Lys Val Gln Glu Leu Ser Phe Lys Ser Lys Pro Asn Val
 450 455 460
 Trp Ala Tyr Phe Ser Val Lys Ser Gly Gly Gly Ile His Glu Phe Ser
 465 470 475 480
 Asp Ser Gln Phe Gly His Val Phe Ala Phe Gly Glu Ser Arg Ala Leu
 485 490 495
 Ala Ile Ala Asn Met Val Leu Gly Leu Lys Glu Ile Gln Ile Arg Gly
 500 505 510
 Glu Ile Arg Thr Asn Val Asp Tyr Thr Ile Asp Leu Leu Asn Ala Ser
 515 520 525
 Asp Tyr Arg Asp Asn Lys Ile His Thr Gly Trp Leu Asp Ser Arg Ile
 530 535 540
 Ala Met Arg Val Arg Ala Glu Arg Pro Pro Trp Tyr Leu Ser Val Val
 545 550 555 560
 Gly Gly Ala Leu Tyr Lys Ala Ser Ala Ser Ser Ala Ala Leu Val Ser
 565 570 575
 Asp Tyr Val Gly Tyr Leu Glu Lys Gly Gln Ile Pro Pro Lys His Ile
 580 585 590
 Ser Leu Val His Ser Gln Val Ser Leu Ser Ile Glu Gly Ser Lys Tyr
 595 600 605
 Thr Ile Asp Met Val Arg Gly Gly Pro Gly Ser Tyr Lys Leu Lys Leu
 610 615 620
 Asn Gln Ser Glu Ile Glu Ala Glu Ile His Thr Leu Arg Asp Gly Gly
 625 630 635 640
 Leu Leu Met Gln Leu Asp Gly Asn Ser His Val Ile Tyr Ala Glu Glu
 645 650 655
 Glu Ala Ala Gly Thr Arg Leu Leu Ile Asp Gly Arg Thr Cys Leu Leu
 660 665 670
 Gln Asn Asp Asp Asp Pro Ser Lys Leu Ile Gly Glu Thr Pro Cys Lys
 675 680 685
 Leu Leu Arg Tyr Leu Val Ala Asp Asp Ser Gln Ile Asp Ala Asp Thr
 690 695 700
 Pro Tyr Ala Glu Val Glu Val Met Lys Met Cys Met Pro Leu Leu Ser
 705 710 715 720
 Pro Ala Ser Gly Ile Ile His Phe Arg Met Ala Glu Gly Gln Ala Met
 725 730 735
 Gln Ala Gly Glu Leu Ile Ala Lys Leu Asp Leu Asp Asp Gly Ser Ala
 740 745 750
 Val Arg Lys Ala Glu Pro Phe Thr Gly Ser Phe Pro Ile Leu Gly Pro

F00240" 246880

755 760 . 765
 Pro Thr Ala Ile Ser Gly Lys Val His Gln Lys Cys Ala Ala Ser Leu
 770 775 780
 Asn Ala Ala Arg Met Ile Leu Ala Gly Tyr Glu His Asn Ile Asp Glu
 785 790 795 800
 Val Val Val Lys Ser Leu Leu Asn Cys Leu Asp Ser Pro Glu Leu Pro
 805 810 815
 Phe Leu Gln Trp Gln Glu Cys Phe Ala Val Leu Ala Thr Arg Leu Pro
 820 825 830
 Lys Asp Leu Arg Asn Glu Leu Glu Ala Lys Tyr Lys Glu Phe Glu Ile
 835 840 845
 Ile Ser Ser Ser Gln Thr Ile Asp Phe Pro Ala Lys Leu Leu Lys Ala
 850 855 860
 Ile Leu Glu Ala His Leu Ser Ser Cys Pro Glu Asn Glu Lys Gly Ala
 865 870 875 880
 Leu Glu Arg Leu Val Glu Pro Leu Thr Ser Leu Val Lys Ser Tyr Glu
 885 890 895
 Gly Gly Arg Glu Ser His Ala His Lys Ile Val Gln Ser Leu Phe Glu
 900 905 910
 Glu Tyr Leu Ser Val Glu Glu Leu Phe Ser Asp Asn Ile Gln Ala Asp
 915 920 925
 Val Ile Glu Arg Leu Arg Leu Gln Tyr Lys Lys Asp Leu Leu Lys Ile
 930 935 940
 Val Asp Ile Val Leu Ser His Gln Gly Val Lys Ser Lys Asn Lys Leu
 945 950 955 960
 Ile Leu Arg Leu Met Asp Lys Leu Val Tyr Pro Asn Pro Ala Ala Tyr
 965 970 975
 Arg Asp Gln Leu Ile Arg Phe Ser Gln Leu Asn His Ile Val Tyr Ser
 980 985 990
 Glu Leu Ala Leu Lys Ala Ser Gln Leu Leu Glu Gln Thr Lys Leu Ser
 995 1000 1005
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 1010 1015 1020
 Thr Glu Asp Gly Glu Asn Ile Asp Thr Pro Lys Arg Lys Ser Ala Ile
 1025 1030 1035 1040
 Asn Asp Arg Met Glu Asp Leu Val Ser Ala Pro Leu Ala Val Glu Asp
 1045 1050 1055
 Ala Leu Val Gly Leu Phe Asp His Ser Asp His Thr Leu Gln Arg Arg
 1060 1065 1070
 Val Val Glu Thr Tyr Ile Arg Arg Leu Tyr Gln Pro Tyr Leu Val Lys
 1075 1080 1085
 Asp Ser Ile Arg Met Gln Trp His Arg Ser Gly Leu Ile Ala Thr Trp
 1090 1095 1100
 Glu Phe Leu Glu Glu Tyr Val Glu Arg Lys Asn Gly Val Glu Asp Lys
 1105 1110 1115 1120
 Thr Leu Val Glu Lys His Ser Glu Lys Lys Trp Gly Val Met Val Val
 1125 1130 1135
 Ile Lys Ser Leu Gln Phe Leu Pro Ala Ile Ile Ser Ala Ala Leu Arg
 1140 1145 1150
 Glu Ala Thr Asn Asn Phe His Asp Pro Leu Lys Ser Gly Ser Gly Asp
 1155 1160 1165
 Ser Ser Asn His Gly Asn Met Met His Ile Gly Leu Val Gly Ile Asn
 1170 1175 1180
 Asn Gln Met Ser Leu Leu Gln Asp Ser Gly Asp Glu Asp Gln Ala Gln
 1185 1190 1195 1200
 Glu Arg Ile Asp Lys Leu Ala Lys Ile Leu Arg Glu Gln Glu Ile Gly
 1205 1210 1215

T00240" 2468850

Ser Ile Ile His Ala Ala Gly Val Gly Asp Ile Ser Cys Ile Ile Gln
 1220 1225 1230
 Arg Asp Glu Gly Arg Ala Pro Met Arg His Ser Phe His Trp Ser Ser
 1235 1240 1245
 Glu Lys Leu Tyr Tyr Val Glu Glu Pro Leu Leu Leu His Leu Glu Pro
 1250 1255 1260
 Pro Leu Ser Ile Tyr Leu Glu Leu Asp Lys Leu Lys Cys Tyr Glu Asn
 1265 1270 1275 1280
 Ile Arg Tyr Thr Pro Ser Arg Asp Arg Gln Trp His Leu Tyr Thr Val
 1285 1290 1295
 Val Asp Thr Lys Pro Gln Pro Ile Gln Arg Met Phe Leu Arg Thr Leu
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 Ile Arg Gln Pro Thr Thr Asn Glu Gly Tyr Ser Ser Tyr Gln Arg Leu
 1315 1320 1325
 Asp Ala Glu Thr Ser Arg Thr Gln Leu Ala Met Ser Tyr Thr Ser Arg
 1330 1335 1340
 Ser Ile Phe Arg Ser Leu Met Gly Ala Met Glu Glu Leu Glu Leu Asn
 1345 1350 1355 1360
 Ser His Asn Thr Thr Ile Lys Ser Glu His Ala His Met Tyr Leu Tyr
 1365 1370 1375
 Ile Ile Arg Glu Gln Gln Ile Asp Asp Leu Val Pro Tyr Ser Lys Lys
 1380 1385 1390
 Ile Asn Ile Glu Ala Gly Gln Glu Glu Thr Thr Val Glu Ala Ile Leu
 1395 1400 1405
 Glu Glu Leu Ala Gln Glu Ile His Ser Ser Val Gly Val Arg Met His
 1410 1415 1420
 Arg Leu Gly Val Phe Val Trp Glu Ile Lys Leu Trp Ile Thr Ala Cys
 1425 1430 1435 1440
 Gly Gln Ala Asn Gly Ala Trp Arg Val Ile Val Asn Asn Val Thr Gly
 1445 1450 1455
 His Thr Cys Thr Val His Ile Tyr Arg Glu Met Glu Asp Ala Thr Thr
 1460 1465 1470
 His Lys Val Val Tyr Ser Ser Val Thr Val Lys Gly Pro Leu His Gly
 1475 1480 1485
 Val Pro Val Asn Glu Asn Tyr Gln Pro Leu Gly Gly Ile Asp Arg Lys
 1490 1495 1500
 Arg Leu Ala Ala Arg Lys Asn Ser Thr Thr Tyr Cys Tyr Asp Phe Pro
 1505 1510 1515 1520
 Leu Ala Phe Gln Thr Ser Leu Glu Gln Ser Trp Ser Ile Gln Gln Thr
 1525 1530 1535
 Gly Ile Gln Arg Ala Asn Asp Lys Asp Leu Leu Lys Val Thr Glu Leu
 1540 1545 1550
 Lys Phe Ser Glu Lys Ala Gly Ser Trp Gly Thr Ser Leu Val Pro Ala
 1555 1560 1565
 Glu Arg Leu Pro Gly Leu Asn Asp Val Gly Met Val Ala Trp Leu Met
 1570 1575 1580
 Glu Met Cys Thr Pro Lys Phe Pro Ser Gly Arg Thr Ile Leu Val Val
 1585 1590 1595 1600
 Ser Asn Asp Val Thr Phe Lys Ala Gly Ser Phe Gly Pro Arg Glu Asp
 1605 1610 1615
 Ala Phe Phe Arg Ala Val Thr Asp Leu Ala Cys Ala Lys Lys Ile Pro
 1620 1625 1630
 Leu Ile Tyr Leu Ala Ala Asn Ser Gly Ala Arg Leu Gly Val Ala Glu
 1635 1640 1645
 Glu Val Lys Ala Cys Phe Lys Val Gly Trp Ser Glu Glu Ser Lys Pro
 1650 1655 1660
 Glu His Gly Phe Gln Tyr Val Tyr Leu Thr Pro Glu Asp Tyr Ala Arg

T00240" 245E00

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Ile Gly Ser Ser Val Met Ala His Glu Leu Lys Leu Glu Ser Gly Glu						
	1685		1690		1695	
Thr Arg Trp Val Ile Asp Thr Ile Val Gly Lys Glu Asp Gly Leu Gly						
	1700		1705		1710	
Val Glu Asn Leu Ser Gly Ser Gly Ala Ile Ala Gly Ala Tyr Ser Arg						
	1715		1720		1725	
Ala Tyr Lys Glu Thr Phe Thr Leu Thr Tyr Val Thr Gly Arg Thr Val						
	1730		1735		1740	
Gly Ile Gly Ala Tyr Leu Ala Arg Leu Gly Met Arg Cys Ile Gln Arg						
	1745		1750		1755	1760
Leu Asp Gln Pro Ile Ile Leu Thr Gly Phe Ser Ala Leu Asn Lys Leu						
	1765		1770		1775	
Leu Gly Arg Glu Val Tyr Ser Ser His Met Gln Leu Gly Gly Pro Lys						
	1780		1785		1790	
Ile Met Ala Thr Asn Gly Val Val His Leu Thr Val Ser Asp Asp Leu						
	1795		1800		1805	
Glu Gly Val Ser Ser Ile Leu Lys Trp Leu Ser Tyr Val Pro Ser His						
	1810		1815		1820	
Val Gly Gly Ala Leu Pro Ile Val Lys Pro Leu Asp Pro Pro Glu Arg						
	1825		1830		1835	1840
Glu Val Glu Tyr Leu Pro Glu Asn Ser Cys Asp Pro Arg Ala Ala Ile						
	1845		1850		1855	
Ser Gly Thr Leu Asp Val Asn Gly Lys Trp Leu Gly Gly Ile Phe Asp						
	1860		1865		1870	
Lys Asp Ser Phe Val Glu Thr Leu Glu Gly Trp Ala Arg Thr Val Val						
	1875		1880		1885	
Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro Val Gly Ile Val Ala Val						
	1890		1895		1900	
Glu Thr Gln Thr Val Met Gln Ile Ile Pro Ala Asp Pro Gly Gln Leu						
	1905		1910		1915	1920
Asp Ser His Glu Arg Val Val Pro Gln Ala Gly Gln Val Trp Phe Pro						
	1925		1930		1935	
Asp Ser Ala Thr Lys Thr Ala Gln Ala Ile Leu Asp Phe Asn Arg Glu						
	1940		1945		1950	
Glu Leu Pro Leu Phe Ile Ile Ala Asn Trp Arg Gly Phe Ser Gly Gly						
	1955		1960		1965	
Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln Ala Gly Ser Thr Ile Val						
	1970		1975		1980	
Glu Asn Leu Arg Thr Tyr Lys Gln Pro Ile Phe Val Tyr Ile Pro Met						
	1985		1990		1995	2000
Met Gly Glu Leu Arg Gly Gly Ala Trp Val Val Val Asp Ser Arg Ile						
	2005		2010		2015	
Asn Ser Asp His Ile Glu Met Tyr Ala Glu Arg Thr Ala Lys Gly Asn						
	2020		2025		2030	
Val Leu Glu Pro Glu Gly Met Ile Glu Ile Lys Phe Arg Thr Arg Glu						
	2035		2040		2045	
Leu Leu Glu Cys Met Arg Arg Leu Asp Gln Gln Leu Ile Asn Leu Lys						
	2050		2055		2060	
Glu Lys Leu Ser Glu Ala Lys Ser Asn Lys Asp Tyr Gly Ala Tyr Asp						
	2065		2070		2075	2080
Ser Leu Gln Gln Gln Ile Arg Phe Arg Glu Lys Gln Leu Leu Pro Leu						
	2085		2090		2095	
Tyr Thr Gln Ile Ala Thr Lys Phe Ala Glu Leu His Asp Thr Ser Leu						
	2100		2105		2110	
Arg Met Lys Ala Lys Gly Val Ile Arg Glu Val Leu Asp Trp Arg Lys						
	2115		2120		2125	

100240" 246860

Ser Arg Ser Val Phe Tyr Gln Arg Leu His Arg Arg Ile Gly Glu His
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 Ser Leu Ile Asn Ile Val Arg Asp Ala Ala Gly Asp Gln Leu Ser Tyr
 2145 2150 2155 2160
 Val Ser Ala Met Asn Leu Leu Lys Glu Trp Tyr Leu Asn Ser Asp Ile
 2165 2170 2175
 Ala Lys Gly Arg Glu Asp Ala Trp Leu Asp Asp Glu Ala Phe Phe Arg
 2180 2185 2190
 Trp Arg Asp Asp Pro Ala Asn Tyr Glu Asp Lys Leu Lys Glu Leu Arg
 2195 2200 2205
 Val Gln Arg Leu Leu Leu Gln Leu Thr Asn Ile Gly Asp Ser Ala Leu
 2210 2215 2220
 Asp Leu Gln Ala Leu Pro Gln Gly Leu Ala Ala Leu Leu Ser Lys Leu
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 Glu Ala Ser Ser Arg Asp Lys Leu Ile Ser Glu Leu Arg Lys Val Leu
 2245 2250 2255
 Gly

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 <223> primer for PCR

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20

<210> 10
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23

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 <212> DNA
 <213> Artificial Sequence

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 <223> representative construct (3' end)

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46

<210> 12
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 <212> DNA
 <213> Artificial Sequence

TC0047.046E0360

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<223> representative construct (3' end)

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ccttttataa aaaaaaaaaa aagaattcct gcagcccggg ggatcc

46

T00240" 2465860